

Figure 1

MKEIAMRNSKRKPEPTPFAGKKLRSTRLRKRAQISPVLVQSPWLWSKQIGVSAASVDSCS	60
DLLADDNVSCGSSRVEKSSNPKKTLLIEEVEVSKPGYNVKETIGDSKFRRITRSYSKLHKE	120
KEGDEIEVSESSCVDNSGAGLRRLNVKGNKINDNDIEISFRRSDVTFAGHVSNRSLNFE	180
SENKESDVSVISGVEYCSKFGSVTGGADNEEIEISKPSFVEADSSIGSAKELKPELEI	240
VGCVSDLACSEKFFSEEVSDSLDDSESSEQRSEIYSQYSDFDYSDYTPSIFFDGSEFSEKS	300
SSDSPISHRSRLYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRFDDEEVEESYLRLRERE	360
RSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLLLDRFLS	420
<u>KGSFKSERTLILVGLASLTLATRIEENQPPVNSIRKRNFTIQNLRYSRHEVVAMEWLQEV</u>	480
<u>LNFKCFTPTTIFNFLWFYLLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVFLA</u>	540
CIEHNKISAYQRVIKVHVRTTDNELPECVKSLDWLLGQ	578

Figure 2

SDS	377	MDN-TGLIPRLRSIMVQWIVKQCSDMGLQQQETLFLGVGLLDRFLSKGSF	424
cyc2b		MAQQFDISDKMRAILIDWLIEVHDKFELMNETLFLTVMNLIDRFLSKQAV	
cyc2a		M-QQIDLNEKMRAILIDWLIEVHDKFELMNETLFLTVMNLIDRFLSKQNV	
Consensus	M	+ ++R+I++ W++ L +ETLFL+V L+DRFLSK	
SDS	425	KSERTLILVGIASTLATRIEE-NQPYNSIRKRNFTIQNLRYSRHEVVA	472
cyc2b		-ARKKLQLVGLVALLACKYEEVSVP---IVEDLVVISDKAYTRTDVLE	
cyc2a		-MRKKLQLVGLVALLACKYEEVSVP---VVEDLVVISDKAYTRNDVLE	
Consensus		+ L LVG+ +L LA + EE P + I Y+R +V+	
SDS	473	MEWLQVEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSLSD	521
cyc2b		MEKIMLSTLQFNMSLPTQYPFLKRFLKAAQSDKKLEILASFLIELALVD	
cyc2a		MEKTMMLSTLQFNISLPTQYPFLKRFLKAAQADKKCEVLASFLIELALVE	
Consensus	ME	- L+F PT + FL +LKAA A E A L +L D	

Figure 3

	SDS	cyc2b	cyc2a	cyc3b	cycD
SDS	100%	34%/52%	34%/52%	28%/49%	21%/42%
cyc2b		100%	87%/92%	40%/60%	21%/43%
cyc2a			100%	46%/64%	22%/43%
cyc3b				100%	22%/41%